

## EXHIBIT 10

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in **BLASTN** program only:

Reward for a match:  Penalty for a mismatch:

☒ Use Mega BLAST Strand option

Open gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter ☒

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
LSUVALSLIDUYGNSFYESTULTHALSSQFMLSISEASUNQLKRSUUMUFGSLNVFHYGWUJ  
LWTWGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHT  
FSLKFSQTYTKLNERYAKNNVSSKNYSQCGEMLFSLQEGFLLTKLVGLYSYGDHNCCHFYT  
QGENLTSQGTFRSQTMGGAFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGETALRF
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
ITLNAVNLVDALGNAYEDFILATSRFFTAIVATINASTVIQFTUNLTNYVFFTHYUQJN  
WTVTWDTETATKTATLWEQTGYSPNERQGPLVPNTLWGAFSDLRAIQNLMDISVNGAD  
YHRGFVWSGLANFLHKSGSDTKRKFRHNSAGYALGVYAKTPSDDIFSA AFCQLFGKDKDY  
LVSKNNANIYAGSLYYQHSIYWSAWQNLQNTIGAEAPLVLNAQLTYCHASNDMKTMTT  
TYAPRKTTYAEIKGDWGNDCFGVELGATVPIQTESLLFDMYSPFLKFQLVHTHQDDFKE  
NNSDQGRYFESSNLTNLSLPIGKIFERFANNDTASYHVTAAYSPDIVRSNPDCCTSLVLS  
PDSAVWVTKANLARSFMLQAGNYLSLSHNIIEIFSQFGFELRGSSRTYNVDLGSKIQF
```

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



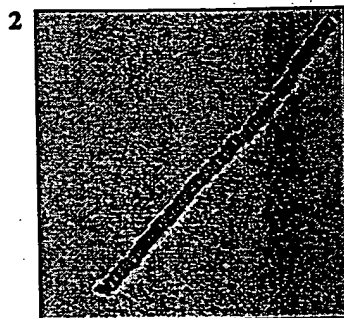
## Blast 2 Sequences results

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ Align

Sequence 1 lc|seq\_1 Length 965 (1..965)

Sequence 2 lc|seq\_2 Length 839 (1..839)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 153 bits (386), Expect = 2e-35

Identities = 201/781 (25%), Positives = 320/781 (40%), Gaps = 114/781 (14%)

```
Query: 189 TFVSENQSCFLFMDNICIQNTAGKGGAIYA-GTSNSFESNCDLFFINNACCAGGAIF 247
      TF+ + CF DNI T TA GAI G + + LF + A C G
Sbjct: 85 TFLGNGYTLCF---DNI---TTTASNPGAINVQGGKTLGISGSLF--SCAYCPPGTTG 136

Query: 248 SPICSLTGN-----RGNIVFYNNRCFKNVETASSEASDGGAIKVTTRLDVT---GNRGRI 299
      GN ++VF+ KN TA +GGAI+ D N +
Sbjct: 137 YGAIQTKGNTTLKDNSSLVFH-----KNCSTA-----EGGAIQCKGSSDAELKIENNQNL 186

Query: 300 FFSDNITKNYGGAIYAPVVTLDVNGPTYFXXXXXXXXX-----XXKXDGTSNSKISADR 354
      FS+N + + GGAIYA +T+V GPT F D + ++AD
Sbjct: 187 VFSSENSSTSKGGAIYADKLTVSGGPTLFSNNSVSNSSPKGGAISIKDSSGECSLTADL 246

Query: 355 HAIIFNENIVTNVNTNANGTSTSANPPRRNAITVASSSGEILLGAGSSQNLIIFYDPIEVSN 414
      I F+ N + + + T T RN+I + + L A + FYDPI
Sbjct: 247 GDITFDGNKIIRKSGSSSTVT-----RNSIDLGTGKFT-KLRAKDGFGIFFYDPIITGGG 299

Query: 415 AG-VVSFNKEADQTSVVFSGATVNSAD-FHQRNLQTKTPAPLTLNGLFCIEDHAQLT 472
      + +++ + D TG +VFSG ++ + NL + P+TSL G L ++D +T
Sbjct: 300 SDELNINKKETVDYTGKIVFSGEKLSDDEEKARAENLASTFNQPIITLSAGSLVLKDGVSVT 359

Query: 473 VNRFTQ-TGGVVSILGNGAVLSCYKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLV 531
      + TQ G V + G L +G +ITL ++ +N++S+ G
Sbjct: 360 AKQVTQEAGSTVMDLGTTLQTPSSGG-----ETITLTNLDINIASLGGGG-----T 407

Query: 532 EPTNNSNNYTADTAATFSLSDVKLSLIDYGNSPYESTDLTHALSSQFMLSISEASDNQL 591
      P + N TA A T + ++L+D GN+ YE L +S+P +I ++
Sbjct: 408 SPAKLATN-TASQAITINA---VNLVDADGNA-YEDPILA---TSKPFTAIVATTNAST 458

Query: 592 RSDDMDPFGSLNVP--HYGWQGLWTGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLP 649
      + D VP HYG+QG WT W D E A+ +T LTW
Sbjct: 459 VTQPTDNLNYPVPPHYGQGNWVTW---DTETAT-----KTATLTWEQ 500

Query: 650 AGYVPSPKHRSPLIANTLWG--NMLLATESLKNSAELTPSDHFFWGITGGGLGMVYQDP 707
      GY P+P+ + PL+ NTLWG + L A ++L + + H G GL +++
Sbjct: 501 TGYSNPNERQGPLVNTLWGAFSDLRAIQNLMDISVNGADYHR--GFWVSGLANFLHKSG 558

Query: 708 RENHPGPHMRSSGYSAGMIA--GQTHTFSLKFSQTYTKLNE-RYAKN--NVSSKNYSCQG 762
```

+ F S+GY+ G+ A FS F Q + K + +KN N+ + + Q  
 Sbjct: 559 SDTKRKFRHNSAGYALGVYAKTPSDDIFSAAFQQLFGKDKDYLVSKNNANIYAGSLYYQH 618  
 Query: 763 EMLFSLQEGFLLTKLVGLYSYGDHN-----CHHFTYQGENLTS-----QGTFR 805  
 +S + LL +G + N CH N+T+ +G +  
 Sbjct: 619 ISYWSAWQN-LLQNTIGAEAPLVNAQLTYCHASNDMKTNTTTTYPKRTTYAEIKGDWG 677  
 Query: 806 SQTMGGAVFFDLPMKPPGSTHI-LTAPFLGALGIYSSLSHFTVEVGAYPRSPSTKTPLINV 864  
 + G + +P++ S + +PFL +++ F E + + L N+  
 Sbjct: 678 NDCPGVELGATVPIQTESLLFDMYSPFLKFQLVHTHQDDFKENNSDQGRYPSSNL/TNL 737  
 Query: 865 LVPIGVKGSMFNATQRPQAWTVELAYQFVLYRQEPGIATQLLAS--KGIWFGSGSPSSRH 922  
 +PIG+K A ++ V AY P + R P T LL S +W + +R  
 Sbjct: 738 SLPIGIKPERF-ANNDTASYHVTAAAYSPDIVRSNPDCTTSLLVSPDSAVWVTKANNLARS 796  
 Query: 923 A 923  
 A  
 Sbjct: 797 A 797

CPU time: 0.21 user secs. 0.04 sys. secs 0.25 total secs.

Lambda K H  
 0.317 0.133 0.397

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 9430

Number of Sequences: 0

Number of extensions: 782

Number of successful extensions: 11

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 965

length of database: 326,943,915

effective HSP length: 134

effective length of query: 831

effective length of database: 281,544,581

effective search space: 233963546811

effective search space used: 233963546811

T: 9

A: 40

X1: 16 ( 7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 78 (34.7 bits)

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

**Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

☒ Use MegaBLAST Strand option

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter ☒

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
LSLVKLSLIDUYGNSFTESLTHALSSQFMLSISEASINQLKSDUDFSGLNVPHYGWG  
LWTWGWAKTQDFEPASSATITDPQKANRFHRTLTLTWLPAGYVSPKHSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQHT  
FSLKFSQTYTTLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFT  
QGENLTSQGTFRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINLVPIGVKGSFMMNATQRPQAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHAMSYSKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
HYGTQSNWIVITWAQSSAQERTATLTIWEQIGTSPNFERQSLVFNLTWGSFSDIKAIQNL  
MDISVNGADYHRGFWSGLGNFLHKSGSDTKRKRHNSAGYALGVYAQTSEDVFSAPFC  
QLFGKDKDYLVSKNSSTVYAGSIYYQHSIYWNWNTLLQNTLGAEAPLVNAQLAYCHAS  
NNMKTMTDTYAPFKTTYSEIKGDWGNDCFGVEFGAKAPIETASLLPDMYSPFVKLQLVH  
AHQDDFKENNSDQGRYPESNNLTNLSMPIGVKLEKFSHKDTASYNLTLAYAPDIVRSNPD  
CTASLLVSPTSAAVWVTKANNLARHAFILQAGNYLALTRNTELFSSQFGFELRGSCRTYNID  
LGSKIQF
```

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



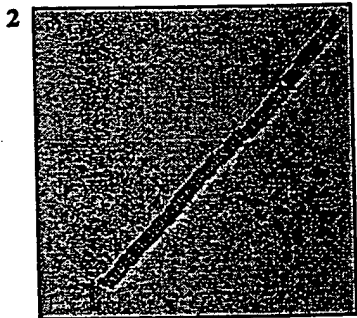
# Blast 2 Sequences results

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter: ☒ **Align**

Sequence 1 lc|seq\_1 Length 965 (1..965)

Sequence 2 lc|seq\_2 Length 847 (1..847)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 165 bits (417), Expect = 4e-39  
Identities = 189/767 (24%), Positives = 308/767 (39%), Gaps = 101/767 (13%)

```
Query: 200 LFMNICTQNTAGKGGAIYAGTSNSFESNNCDLFFINNACCAGGAIFSPICSLTGN--- 256
      L DNI T ++ G +GT+ ++ + LF + A C GA GN
Sbjct: 97 LCFDNIT--TQSSHPGAISVSGTNKTLDISGFSLF--SCAYCPPGATGYGAIKAVGNTTI 152

Query: 257 --RGNIVFYNNRCFKNVETASSEADGGAIKVTTRLDTGNRGRIFSDNITKNYGGAIY 314
      ++VF+ KN T A A L + N+ +F ++N ++ GGAIY
Sbjct: 153 KDNSSLVFH-----KNCSTGEGGAIQCKASSSEAEKLIENNQNLFV-AENSSSSSGGAIY 206

Query: 315 APVVTLLVDNGPTYFXXXXXXXXXXXXX----DGTNSKISADRHAIFNENIVTNVINA 370
      A +T+V GPT F D ++AD I F+ N +
Sbjct: 207 ADKLTIVSGGPTLFSNNSVSASSPKGGAICIKDSGGECSLTADLGDTITFDGKIIKTNGG 266

Query: 371 NGTSTSANPPRRNAITVASSSGEILLGAGSSQNLI FYDPIEVS NAGVSVSFNKE--ADQT 428
      + T T RN+I + SS L A + FYDPI ++ NK+ D T
Sbjct: 267 SPTVT-----RNSIDLSSGKFTKLNAKEGFGIFFYDPI-TGGGSELDNINKQDVTVDYT 319

Query: 429 GSVVFSGATVNSADFH-QRNLTQTKTPAPLTLNGLFCIEDHAQLTVNRFTQT-GGVVSLG 486
      G +VPSG ++ + NL++ PL + +G L ++D L FTQT G V +
Sbjct: 320 GKIVFSGERLSDEEKVAA NLKSDFKQPLKIGSGSLILKDGVTLETQSFTQTGEGATVVM 379

Query: 487 NGAVLSCYKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLWVEPTNNSNNTADTAA 546
      G L +G +ITL ++ +N++S+ G VET S T +
Sbjct: 380 LGTTLQTTPSSGG-----ETITLTNLDINVASLGGGVAPDPKVEATTESKTVTINA-- 431

Query: 547 TFSLSDVKLSLIDYGNSPYESTDLTHALSSQPMLSIS--EASDNQLRSDMDPFGSLNVP 604
      ++L+DD GN+ YE L +SQP +I S + + P
Sbjct: 432 -----VNLVDDNGNA-YEYPILA---ASQPFTAIEVRSGSSGSIKPTTNLENTYTP 479

Query: 605 -HYGWQGLWTGWAKTQDPEPASSATITDPQKANRFHRTLLLTLWPAGYVPSPKHRSPLI 663
      HYG+QG WT W + SSA +T LTW GY P+P+ + L+
Sbjct: 480 THYGYQGNWTVTWKQ-----GSSAQ-----EKTATLTWEQTGYSPNPERQGS 523

Query: 664 ANTLWGNMLLATESLKNSAELTPSDHPFW-GITGGGLGMMVYQDPRENHPGFHMRSSGYS 722
      NTLWG+ +++N +++ + + G GLG +++ + F S+GY+
Sbjct: 524 PNTLWGS-PSDIRAIQNLMDISVNGADYHRGFWVSGLG N FLHKSGSDTKRKFPHNSAGYA 582

Query: 723 AGMIA--GQHTFSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLF-----SLQE 770
```

G+ A FS F Q + K ++ Y + SS Y+ G + + +L +  
Sbjct: 583 LGVYAQTPESEVFSAAFCQLFGK-DKDYLVSKNSSTVYA--GSIYYQHISYWNTWNTLLQ 639  
Query: 771 GFLLTGLVGLYSYGDHNCCHFYTOGENLTS-----QGTFRSQTMGGAFFDLF 818  
L + + + CH N+T +G + + G P  
Sbjct: 640 NTLGAEAPLVLAQLAYCHASNMMKTMTDTYAPPKTTYSEIKGDWGNDCFGVEFGAKAP 699  
Query: 819 MKPFGSTHILTAPFLGALGIYSSLSHPTVEGAYPRSPSTKTPLINVLVPIGVKGSFMNAT 878  
++ + +PF+ +++ F E + + L N+ +PIGVK +  
Sbjct: 700 IETASLLPDMYSPFVKLQLVHAHQDDFKENNSDQGRYFESNNLTNLSMPIGVKLEKF-SH 758  
Query: 879 QRPQAWTVELAYQFVLYRQEPGIATQLLAS--KGIWFGSGSPSSRHA 923  
+ + + LAY P + R P LL S +W + +RHA  
Sbjct: 759 KDTASYNLTLAYAPDIVRSNPDCTASLLVSPTSASVWVTKANNLARHA 805

CPU time: 0.22 user secs. 0.03 sys. secs 0.25 total secs.

Lambda K H  
0.317 0.133 0.397

Gapped  
Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 9976

Number of Sequences: 0

Number of extensions: 824

Number of successful extensions: 14

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 965

length of database: 326,943,915

effective HSP length: 134

effective length of query: 831

effective length of database: 281,544,581

effective search space: 233963546811

effective search space used: 233963546811

T: 9

A: 40

X1: 16 ( 7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 78 (34.7 bits)

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#).  
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

☒ Use Mega BLAST Strand option

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter ☒

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
LSIVRLSLIDUIGNSPIESTULTHALSSQFRLSISEASLNQLKSDUMDFDGLNVFHYGWQJ  
LWTGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMVYQDPRENHPGFHMRSSGYSAGMLAQTHT  
FSLKFSQTYTKLNERVAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFT  
QGENLTSQGTFRSQTMGGAVFFDLPMKPPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINLVPIGVKGSFPMNATQRPQAWTVELAYQFVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHAMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGETALRF
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
DLISVNGAUIISRGFWVSSLANFLNAGSUTAKKAFKHSAGIALGVIAQTFSDDVCSAFCQ  
LFGKDKDYFVSKNSSTIYAGSIYYQHSYWNWTNTLLQNTLGAEAPLVLAQLTYCHASN  
NMKTNMTNTYTPKNVTPSEIKGDWGNDCFGVEFGAKAPIETASLLFDMYSPPVKLQLVHA  
HQDDFKENNSDQGRYFESNNLTNLSMPIGVKLEKFSHKDTASYNLTLAYAPDIVRSNPD  
TASLLVSPTSASVWVTKANLARHAFILQAGNYLALTRNTELSQFGFELRGSCRTYNIDL  
GSKIQF
```

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)

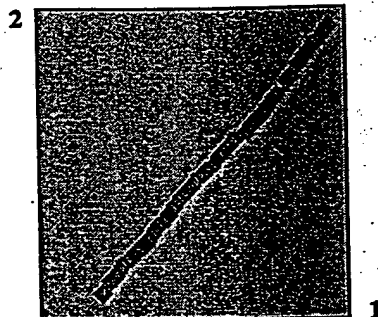




## Blast 2 Sequ nces results

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Alien**

Sequence 1 **lc|seq\_1** Length 965 (1..965)Sequence 2 **lc|seq\_2** Length 846 (1..846)

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 151 bits (382), Expect = 5e-35  
Identities = 184/790 (23%), Positives = 312/790 (39%), Gaps = 101/790 (12%)

```
Query: 182 GAISTANTFVSENGSCFLFMDN---IC---IQTNAGKGGAIYAGTSNSFESNNCDLFF 235
      G S N SE F+ N +C I T ++ G +GT+ + + + LF
Sbjct: 68 GKDSPLNKSCFSETTENLSPIGNGYTLCPDNITTQSSHPGAISVSGTNKTLDISGFSLFS 127

Query: 236 INNACCAG---GAIFSPICSLTGNRGNIVFYNNRCFKNVETASSEASDGGAIKVTTRLD 291
      C G GAI + + + ++VF+ KN TA A + T L
Sbjct: 128 CAYCCPPGTTGYGAIQTKGTTTLKDNSSLVFH-----KNCSTAEGGAIQCKSSSSTAELK 182

Query: 292 VTGNRGRIFSDNITKNGYGAIVPVVTLVDNGPTYFXXXXXXXXXXXXXXXXXX-----DGTS 346
      + N+ +F S+N +K GGAIYA +T+V GPT F D
Sbjct: 183 LENNKNLVLF-SENSSKEKGGAIYADKLTIVSGGPTLFSNNSVSHNSSPKGGAICIKDSGD 241

Query: 347 NSKISADRHAIIFNENIVTNVNTANGTSTSANPPRRNAITVASSSGEILLGAGSSQNLIF 406
      ++A+ I F+ N + + T T RN+I + S L A + F
Sbjct: 242 ECLSLTANLGDITFDGNKIITNGGSPVT-----RNSIDLGGGKFTKLNKEGFGIFF 295

Query: 407 YDPIEVSNAGVSVSFNK---EADQTSVVFSGATVNSADFH-QRNLQTKTPAPLTLNNGF 462
      YDPI + + NK + TG +VFSG ++ + NL++ PL + G
Sbjct: 296 YDPIANTGGSTEIELNKTESDITYTGRIVFSGEKLSDDEKTPANLKSIFYKQPLKIGAGS 355

Query: 463 LCIEDHAQLTVNRFTQT-GGVVSLGNGAVLSCYKNGAGNSASNASITLKHIGLNLSSILK 521
      L ++D L + TOT G V + G L S+S +ITL ++ +N++S+
Sbjct: 356 LVLKDGVTLEAKKITQTKGSTVVMDLGTTLQT-----PSSSGETITLTNLDINIASLGG 409

Query: 522 SGAEIFLLWVEPTNNSNNYTDATATFSLSDVKLSLIDYGNISPYESTDLTHALSSQPM 581
      G P A A+ ++S ++L++ N+ YE L+ + S +
Sbjct: 410 GGGTAPAK-----LATNTASQAISIAAVNLVNTDSNT-YEDPILSASKSFSAIT 457

Query: 582 SISEASDNQLRSDMDDFSGLNVP-HYGWQGLWTGWAKTQDPEPASSATITDPQKANRFH 640
      ++ +S + + + P HYG+QG WT W + SSA
Sbjct: 458 ATTSSST--VTPPETNLKNYTPPTHYGYQGNWTVTWKQ-----GSSAQ-----E 499

Query: 641 RTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSELTSPSDHPF-WGITGGGL 699
      +T LTW GY P+P+ L+ NTLWG T +++N +++ + G L
Sbjct: 500 KTATLTWEGTGYSPNPERVGSGLVPNTLWG-AFSDTRAIQNLMDISVNGADYSRGFWVSSL 558
```

Query: 700 GMMVYQDPRENHPGFHMRSSGYSAGMIA--GQTHTFSLKFSQTYTKLNERYAKNNVSSKN 757  
 ++ + F S+GY+ G+ A S F Q+ K++ N SS  
 Sbjct: 559 ANFLNKSQSDTKRKFRHHSAGYALGVYAQTPSDDVCSAAFCQLFGKDKDYFVSKN-SSTI 617

Query: 758 YSCQGEMLF-----SLQEGFLITKLVLGLYSYGDHNCCHFYTQGENLTS----- 800  
 Y+ G+ + +L+ L+ + + CH N+T+  
 Sbjct: 618 YA--GSIYYQHISYWNWNTLLQNTLGAEAPLVNLNAQLTYCHASNMMKTNNMTNTYTPKNV 675

Query: 801 -----QGTFRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHPTVEVGAYPRSP 855  
 +G+ + G P++ + +PF+ +++ FE + +  
 Sbjct: 676 TPSEIKGDWGNDCFGVEFGAKAPIETASLLFDMYSPFVKLQLVHAHQDDFKENNSDQGRY 735

Query: 856 STKTPLINVLVPIGVKGSFMNATQRPQAWTVELAYQFVLYRQEPGIATQLLAS--KGIWF 913  
 L N+ +PIGVK + + ++ + LAY P+ R P LL S +W  
 Sbjct: 736 FESNLTNLSPMIGVKLEKF-SHKDTASYNLTLAYAPDIVRSNPDCTASLLVSPTS AVVW 794

Query: 914 GSGSPSSRHA 923  
 + +RHA  
 Sbjct: 795 TKANNLARHA 804

CPU time: 0.25 user secs. 0.03 sys. secs 0.28 total secs.

Lambda K H  
 0.317 0.133 0.397

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

# Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 9987

Number of Sequences: 0

Number of extensions: 805

Number of successful extensions: 11

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 965

length of database: 326,943,915

effective HSP length: 134

effective length of query: 831

effective length of database: 281,544,581

effective search space: 233963546811

effective search space used: 233963546811

T: 9

A: 40

X1: 16 ( 7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 78 (34.7 bits)